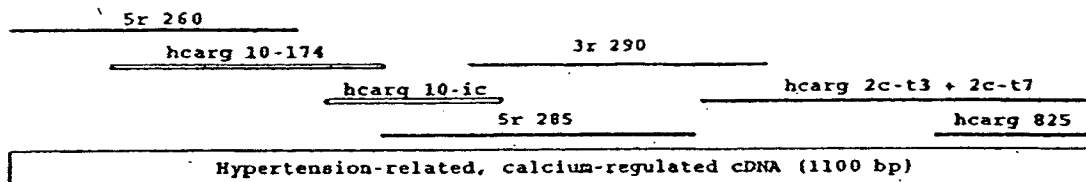


A



B

-131

GTAAAGGCTTGGTTTGTATTGTAAATGCAACTGTGGTTAGGACCTTCTCTCGGACTGGTCAAGAAACGGGAAGAAAGG -80
 -1
 ATG TCT GCT TTG GGG GCT GCA GCT CCA TAC TTG CAC CAT CCC GCT GAC AGT CAC AGT GGC 60
 Met Ser Ala Leu Gly Ala Ala Pro Tyr Leu His His Pro Ala Asp Ser His Ser Gly

CGG GTC AGT TTC CTG GGT TCC CAG CCC TCT CCA GAA GTG ACG GCC GTG GCT CAG CTC TTG 120
 Arg Val Ser Phe Leu Gly Ser Gln Pro Ser Pro Glu Val Thr Ala Val Ala Gln Leu Leu

AAG GAC TTA GAC AGG AGC ACC TTC AGA AAG TTG TTG AAA CTT GTA GTC GGG GCC CTG CAT 180
 Lys Asp Leu Asp Arg Ser Thr Phe Arg Lys Leu Leu Lys Leu Val Val Gly Ala Leu His

GGG AAA GAC TGC AGA GAA GCT GTG GAG CAA CTT GGT GCC AGC GCC AAC CTG TCA GAA GAG 240
 Gly Lys Asp Cys Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu Ser Glu Glu

CGT CTG GCC GTC CTG CTG GCG GGC ACA CAC ACC CTG CTC CAG CAG GCT CTC CGG CTG CCC 300
 Arg Leu Ala Val Leu Leu Ala Gly Thr His Thr Leu Leu Gln Gln Ala Leu Arg Leu Pro

CCT GCT AGT CTA AAG CCA GAT GCC TTC CAG GAA GAG CTC CAG GAA CTT GGC ATT CCT CAG 360
 Pro Ala Ser Leu Lys Pro Asp Ala Phe Gln Glu Glu Leu Gln Glu Leu Gly Ile Pro Gln

GAT CTA ATT GGA GAT TTG GCC AGT TTG GCA TTT GGG AGT CAA CGC CCT CTT CTC GAC TCT 420
 Asp Leu Ile Gly Asp Leu Ala Ser Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser

GTA GCC CAA CAG CAG GGA TCC TCG CTG CCT CAC GTG TCT TAC TTC CGG TGG CGG GTG GAC 480
 Val Ala Gln Gln Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp Arg Val Asp

GTG GCC ATC TCA ACC AGC GCT CAG TCC CGC TCC CTG CAA CCG AGT GTT CTC ATG CAG CTG 540
 Val Ala Ile Ser Thr Ser Ala Gln Ser Arg Ser Leu Gln Pro Ser Val Leu Met Gln Leu

AAG CTC ACA GAT GGA TCT GCA CAC CGC TTC GAG GTG CCC ATA GCC AAA TTT CAG GAG CTG 600
 Lys Leu Thr Asp Gly Ser Ala His Arg Phe Glu Val Pro Ile Ala Lys Phe Gln Glu Leu

CGG TAC AGT GTA GCC TTG GTC CTT AAG GAG ATG GCA GAA CTG GAG AAG AAG TGT GAG CGC 660
 Arg Tyr Ser Val Ala Leu Val Leu Lys Glu Met Ala Glu Leu Glu Lys Lys Cys Glu Arg

AAA CTG CAG GAC TGA CTGAACCTGGTACTGTGGGTGCTGAACCTGGTACCAGAACACAGCCCCCACTGGTGA 734
 Lys Leu Gln Asp TER

TGAGCCCAACTCCATTGAGGTCTGTCATGTGAGAACGTATTTAAGTGAAAAGACAGCGGGACTTTTCAGGTTTTGTTTT 813
 ATCAGTCAACAGCTGGGCAGGGTGGCAGAGTTTATAATCTCAGCCCTTGGAAAGTCTGAGGCTGGAGAATGGGAAGTGTA 892
 AGCTGGCCCTGGCTTTCATAGTGAGGCTCAGTGTGCAATTAAAGAGGTAAAGCAACTATTAAAAA 969

FIGURE 1

005240" 89540650

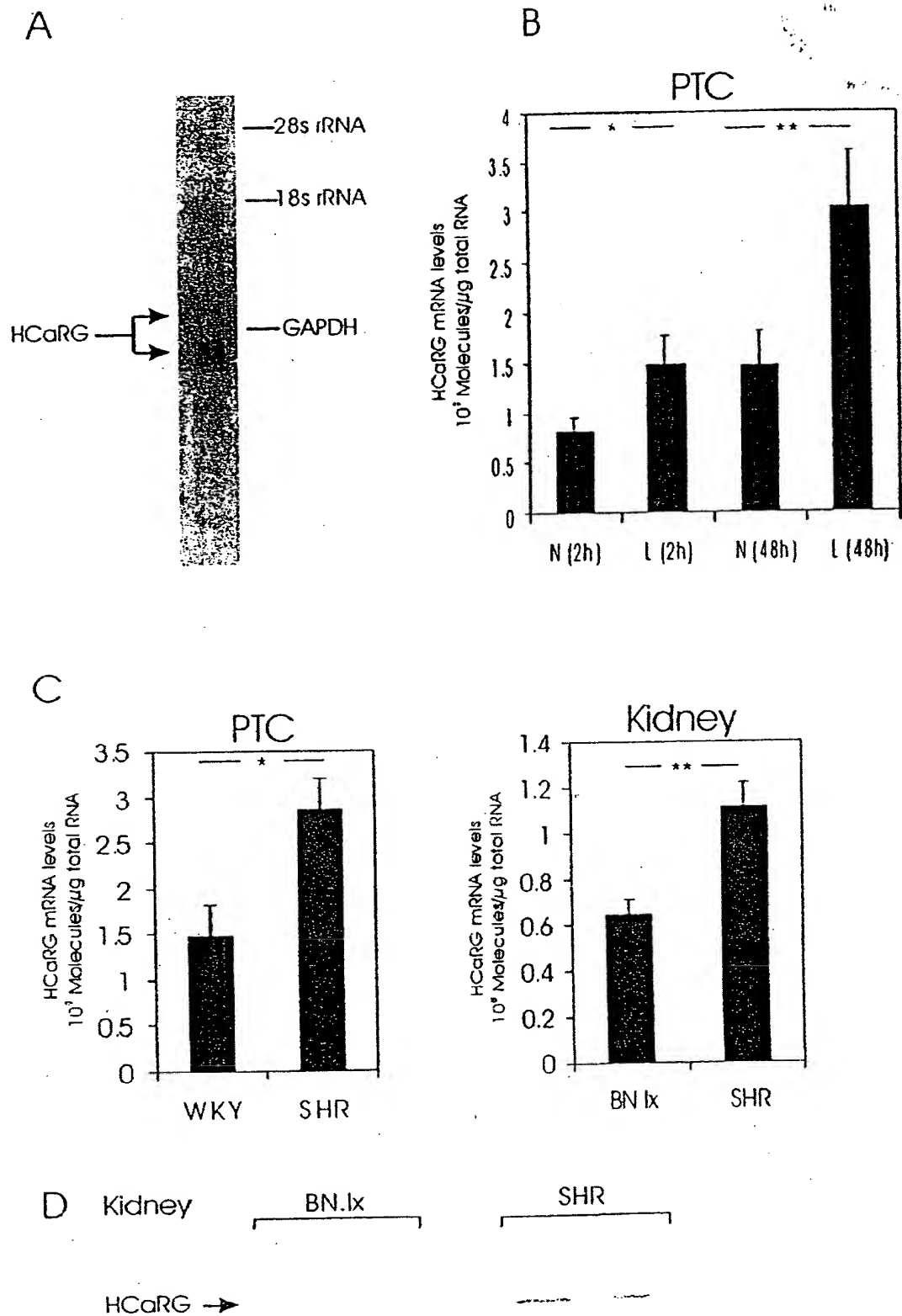


FIGURE 2

0904568-042502

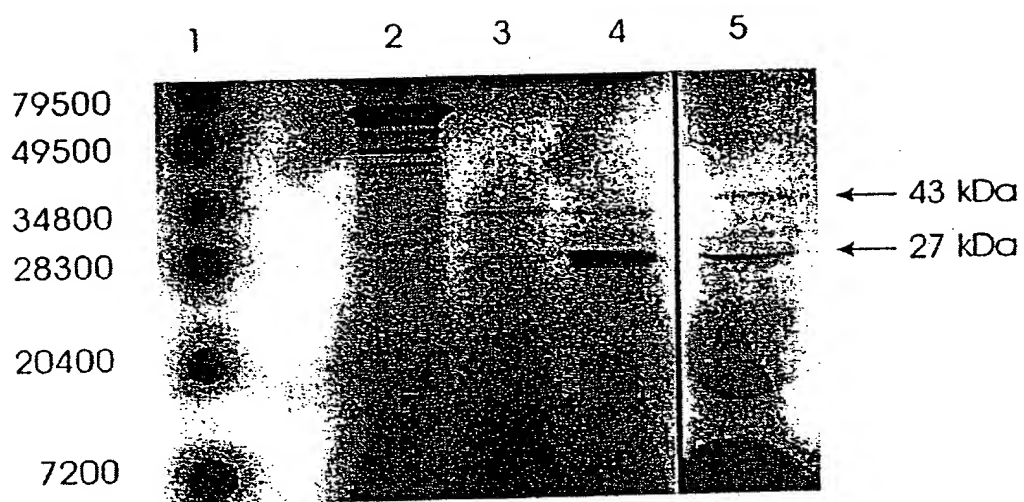


FIGURE 3

rHCaRG	MSA	IGAA	APY	HHHA	DSH	CH	RYS	SS	OPS	PEV	IA	QA	LL	KD	DR	SR	ER	KK	50
hHCaRG	MSA	IGAA	APY	HHHA	DSH	CH	RYS	SS	OPS	PEV	IA	QA	LL	KD	DR	SR	ER	KK	50
rHCaRG	LLK	IV	GA	TH	GK	CREA	VEQ	LG	SAN	ISEE	RL	AV	LL	AG	TH	TU	CO	NR	100
hHCaRG	LLK	IV	GA	TH	GK	CREA	VEQ	LG	SAN	ISEE	RL	AV	LL	AG	TH	TU	CO	NR	100
rHCaRG	PAS	LK	PD	AF	Q	EEL	QEL	GI	PQ	DI	IG	DL	AS	LA	FG	SQ	RP	LL	150
hHCaRG	ETS	LK	PD	TH	R	DQ	QEL	GI	PQ	DI	IG	DL	AS	VV	FG	SQ	RP	LL	150
rHCaRG	HVS	YF	RW	RV	VD	VA	IST	S	AQ	SR	SL	QPS	V	L	M	Q	L	K	200
hHCaRG	HVA	D	F	R	W	RV	VD	VA	IST	S	AQ	SR	SL	QPS	V	L	M	Q	200
rHCaRG	RYS	V	A	L	V	L	K	E	M	A	E	L	E	K	K	C	E	R	224
hHCaRG	RYS	V	A	L	V	L	K	E	M	A	E	L	E	K	K	C	E	R	224

FIGURE 4

09904568.042502

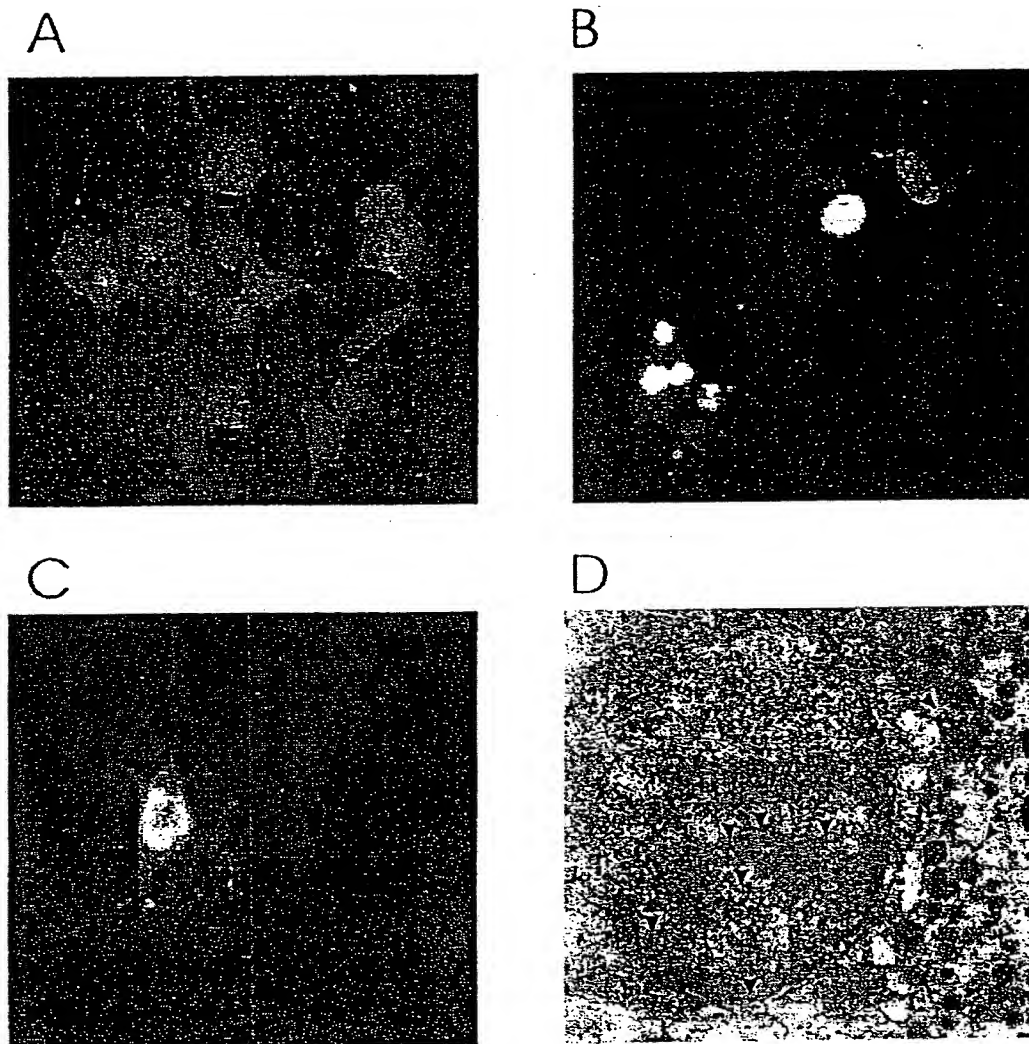


FIGURE 5

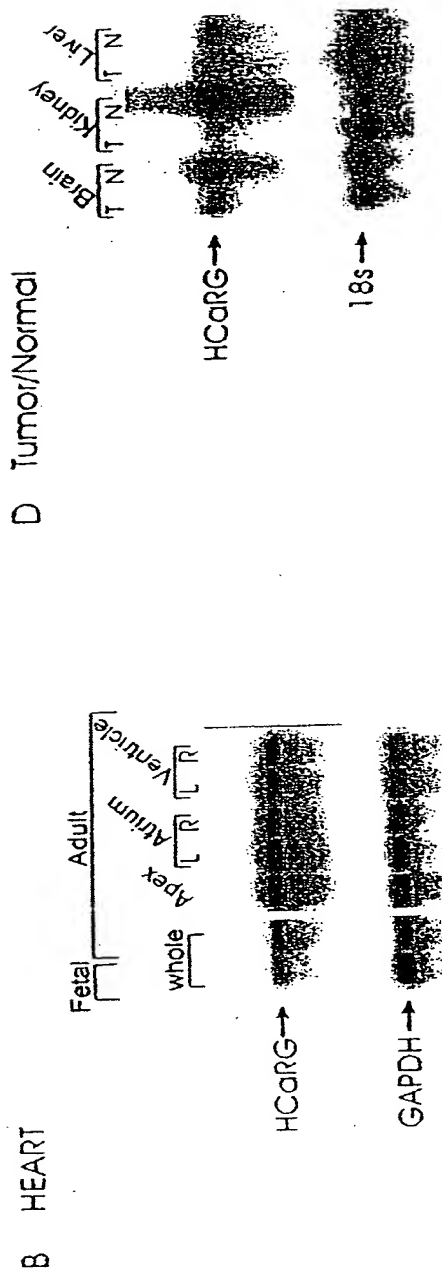
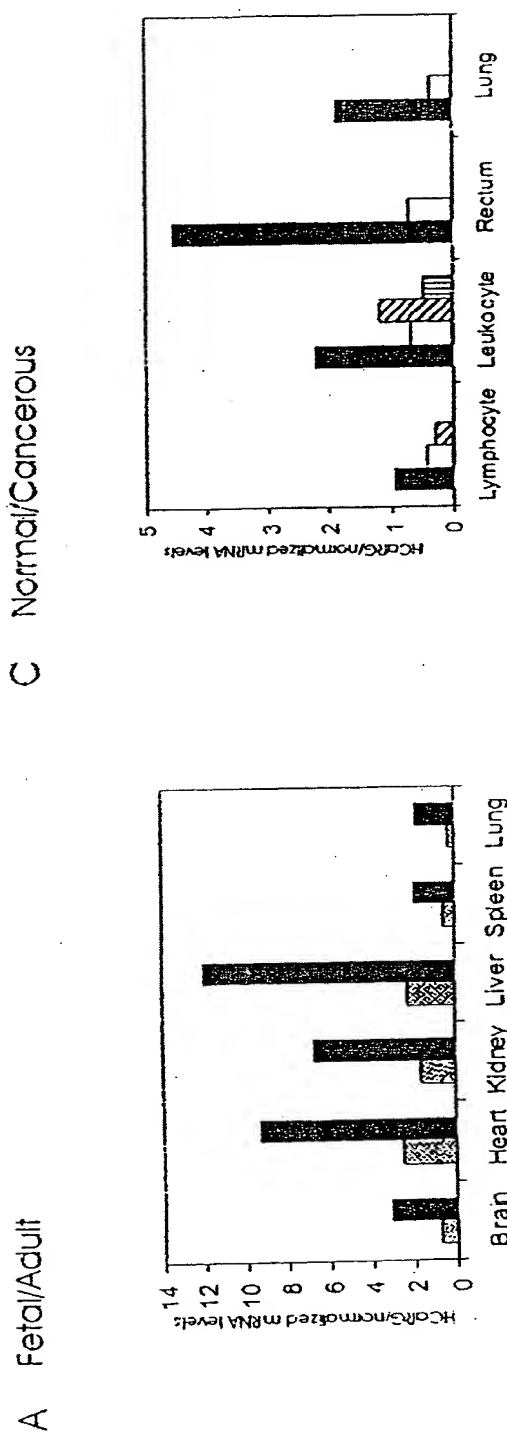


FIGURE 6

09904568-042500

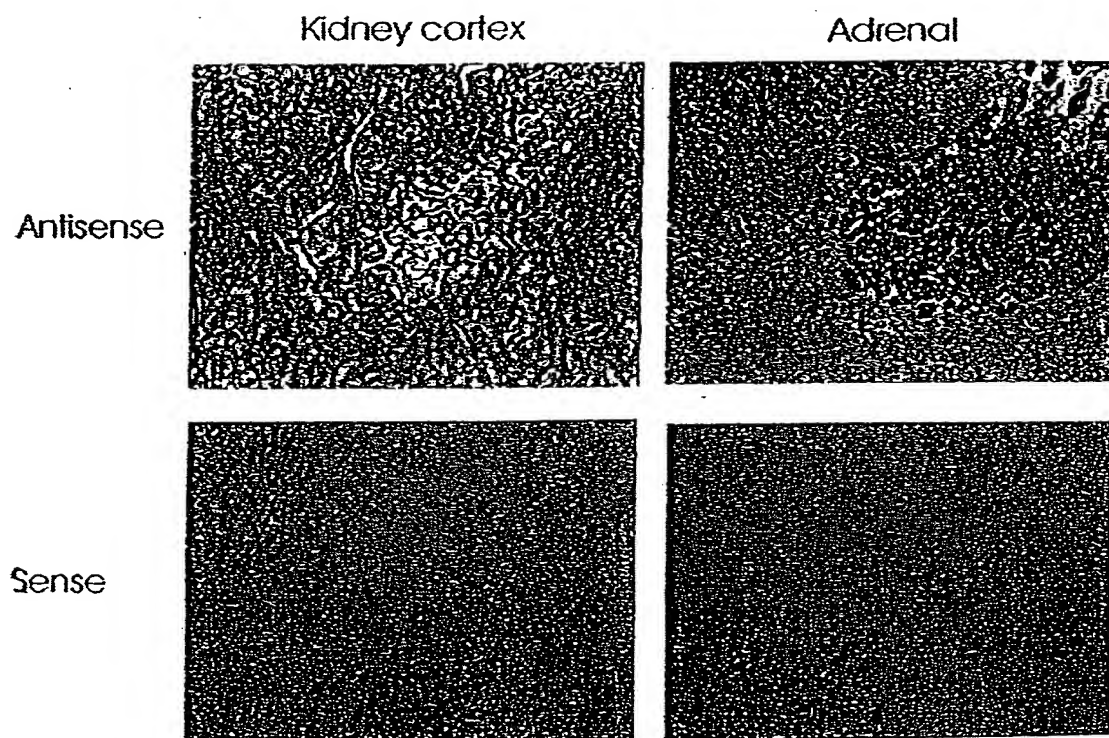
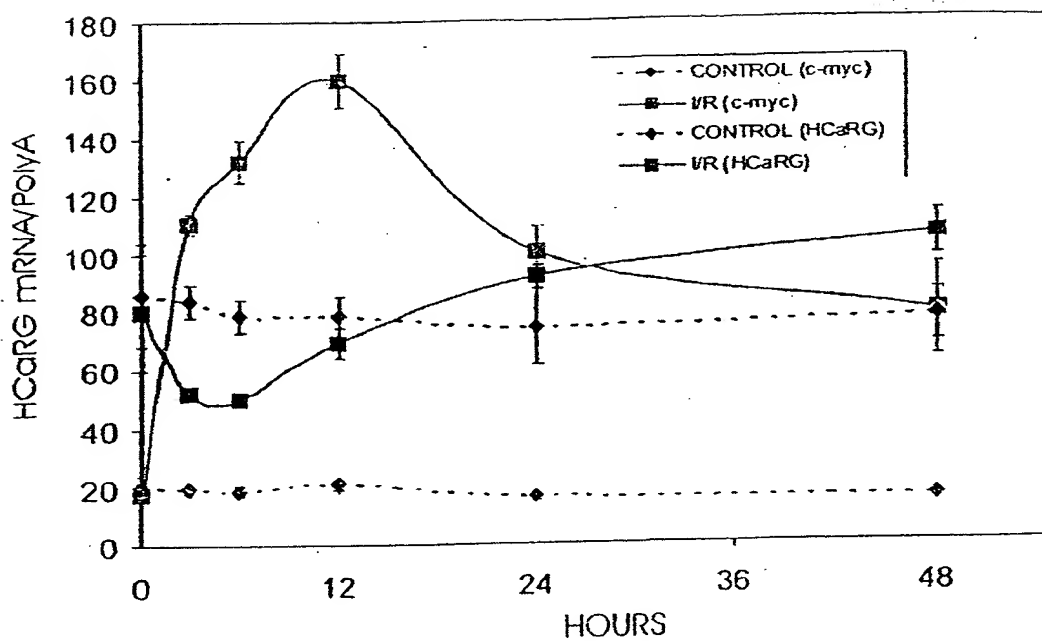
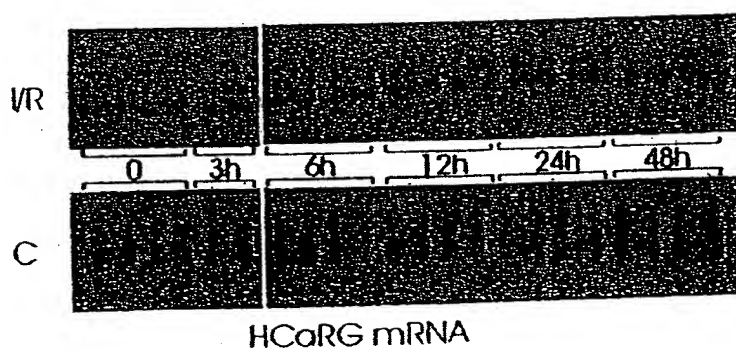


FIGURE 7

A Medulla



B Cortex



C Cortex

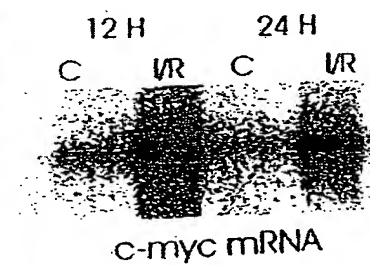
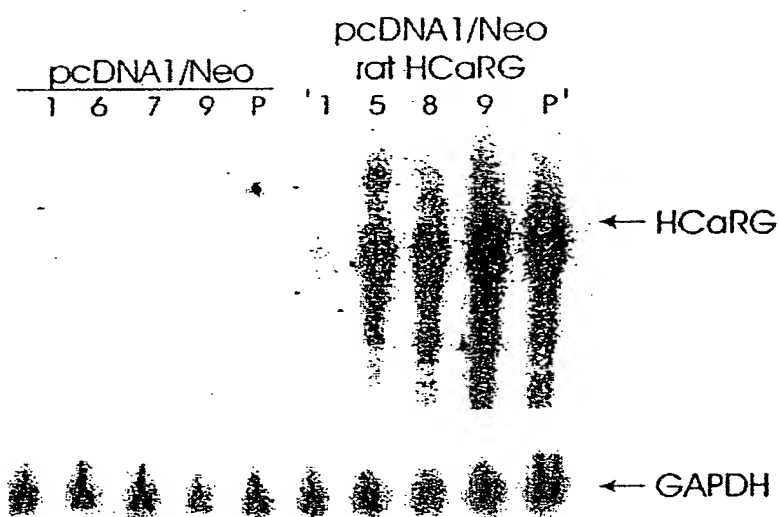


FIGURE 8

A



B

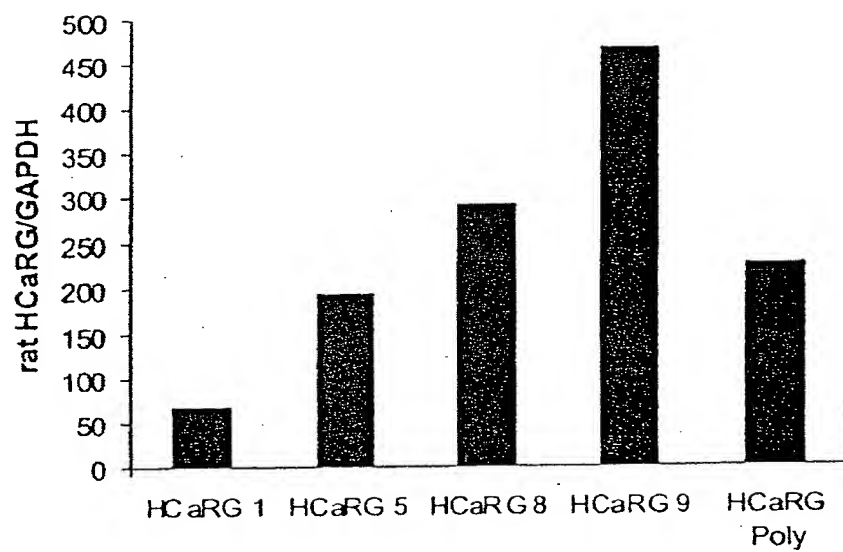
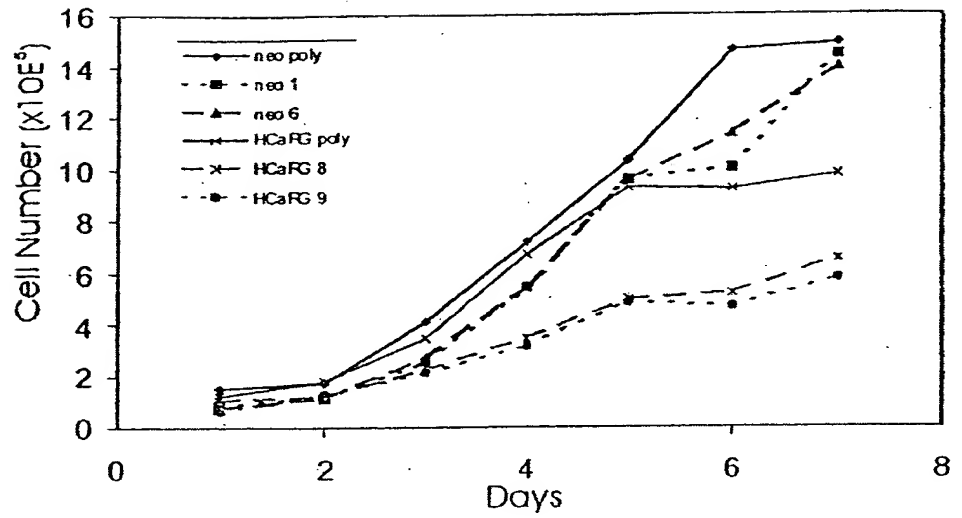


FIGURE 9

205240 89540660

A



B

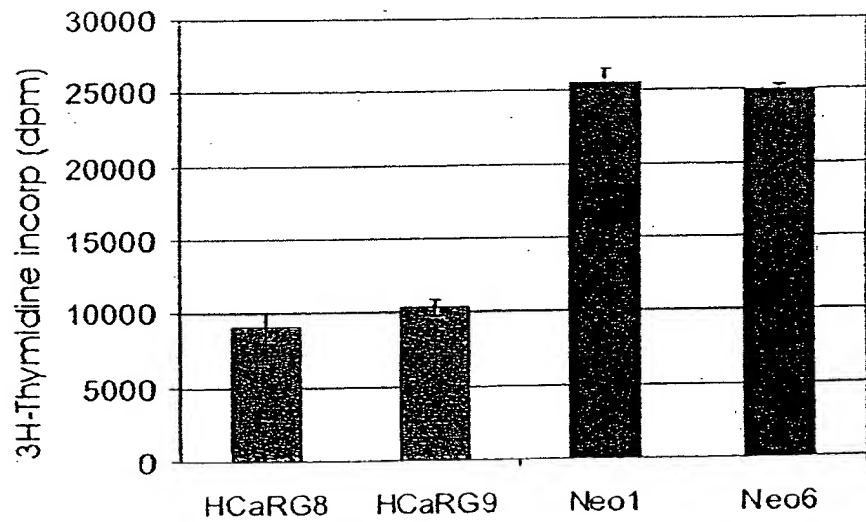


FIGURE 10

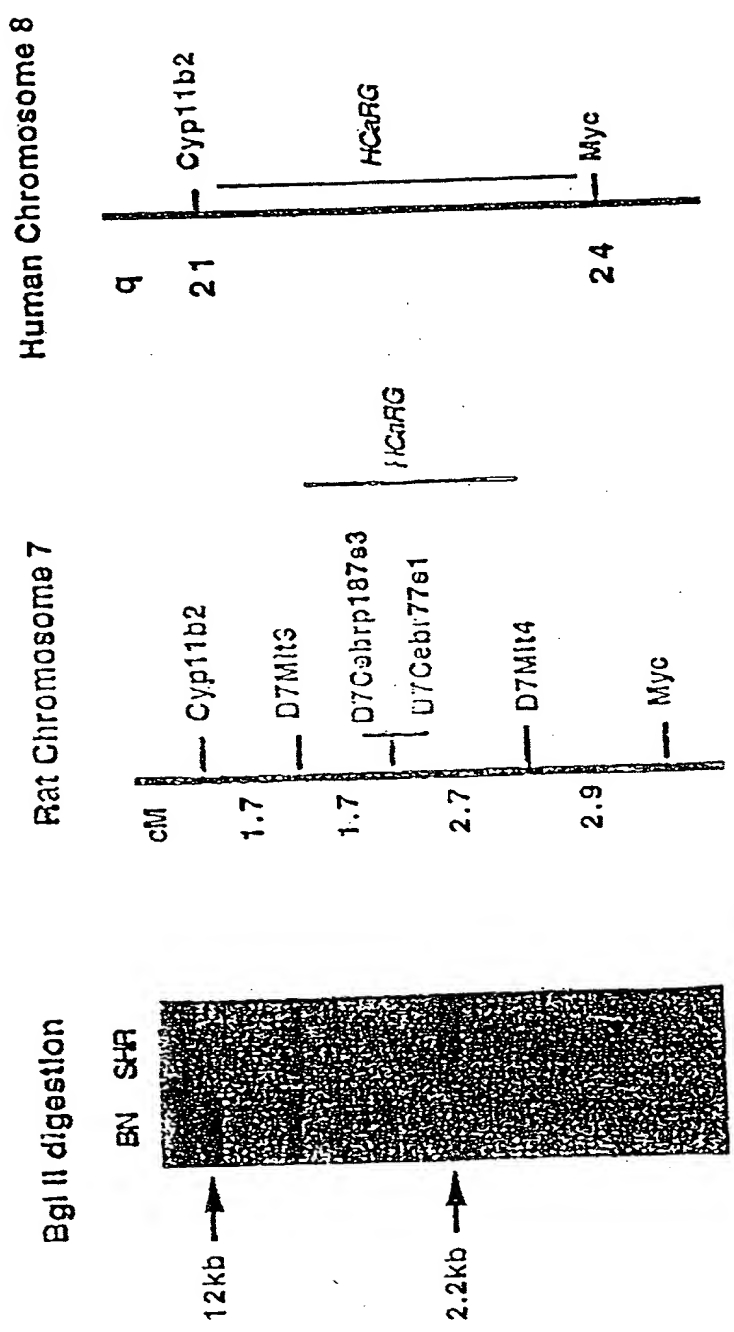


FIGURE 11